

09340690-062999

10 30 50
GCACGAGCTGCCTCCCGCAGGCGCCACCTGTGTCCCCCAGCGCCGCTCCACCCAGCAGGC
70 90 110
CTGAGCCCCCTCTCTGCTGCCAGACACCCCTGCTGCCCACTCTCCTGCTGCTCGGGTTCT
130 150 170
GAGGCACAGCTTGTACACCGAGGCGGATTCTCTTTCTCTTTCTTTCTTTCTTTCTGGCCC
190 210 230
ACAGCCGCAGCAATGGCGCTGAGTTCTCTGCTGGAGTTCATCCTGCTAGCTGGGTTCCT
250 270 290
GAGCTGCCGGTCTGAGCCTGAGGCATGGAGCCTCCTGGAGACTGGGGGCCTCCTCCCTGG
310 330 350
AGATCCACCCCCAAAACCGACGTCTTGAGGCTGGTGTGTATCTCACCTTCCTGGGAGCC
R S T P K T D V L R L V L Y L T F L G A
370 390 410
CCCTGCTACGCCCCAGCTCTGCCGTCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAG
P C Y A P A L P S C K E D E Y P V G S E
430 450 470
TGCTGCCCCAAGTGCAGTCCAGTTATCGTGTGAAGGAGGCCTGCGGGGAGCTGACGGGC
C C P K C S P G Y R V K E A C G E L T G
490 510 530
ACAGTGTGTGAACCCTGCCCTCCAGGCACCTACATTGCCCACCTCAATGGCCTAAGCAAG
T V C E P C P P G T Y I A H L N G L S K
550 570 590
TGTCTGCAGTGCCAAATGTGTGACCCAGCCATGGGCCTGCGCGCGAGCCGGAAGTCTCC
C L Q C Q M C D P A M G L R A S R N C S
610 630 650
AGGACAGAGAACGCCGTGTGTGGTTGCAGCCCAGGCCACTTCTGCATCGTCCAGGACGGG
R T E N A V C G C S P G H F C I V Q D G
670 690 710
GACCACTGCGCCGCGTGCCGCGCTTACGCCACCTCCAGCCCGGGCCAGAGGGTGCAGAAG
D H C A A C R A Y A T S S P G Q R V Q K
730 750 770
GGAGGCACCGAGAGTCAGGACACCCCTGTGTGAGAACTGCCCCCGGGGACCTTCTCTCCC
G G T E S Q D T L C Q N C P P G T F S P
790 810 830
AATGGGACCCCTGGAGGAATGTCAGCACCAGACCAAGTGCAGCTGGCTGGTGACGAAGGCC
N G T L E E C Q H Q T K C S W L V T K A
850 870 890
GGAGCTGGGACCAGCAGCTCCCACTGGGTATGGTGGTTTCTCTCAGGGAGCCTCGTCATC
G A G T S S S H W V W W F L S G S L V I
910 930 950
GTCATTGTTTGTCTCCACAGTTGGCCTAATCATATGTGTGAAAAGAAGAAAGCCAAGGGGT
V I V C S T V G L I I C V K R R K P R G
970 990 1010

Figure 1A

09240690-062999

GATGTAGTCAAGGTGATCGTCTCCGTCCAGCGGAAAAGACAGGAGGCAGAAGGTGAGGCC
D V V K V I V S V Q R K R Q E A E G E A
1030 1050 1070
ACAGTCATTGAGGCCCTGCAGGCCCCCTCCGGACGTCACCACGGTGGCCGTGGAGGAGACA
T V I E A L Q A P P D V T T V A V E E T
1090 1110 1130
ATACCCTCATTACGGGGAGGAGCCCCAAACCACTGACCCACAGACTCTGCACCCCCGACGC
I P S F T G R S P N H *
1150 1170 1190
CAGAGATACCTGGAGCGACGGCTGAATGAAAGAGGCTGTCCACCTGGCGGAACCACCGGA
1210 1230 1250
GCCCCGAGGCTTGGGGGCTCCACCCTGGACTGGCTTCCGTCTCCTCCAGTGGAGGGAGAG
1270 1290 1310
GTGGCGCCCCTGCTGGGGTAGAGCTGGGGACGCCACGTGCCATTCCCATGGGCCAGTGAG
1330 1350 1370
GGCCTGGGGCCTCTGTTCTGCTGTGGCCTGAGCTCCCCAGAGTCCTGAGGAGGAGCGCCA
1390 1410 1430
GTTGCCCCCTCGCTCACAGACCACACACCCAGCCCTCCTGGGCCAACCCAGAGGGCCTTCA
1450 1470 1490
GACCCAGCTGTGTGCGCGTCTGACTCTTGTGGCCTCAGCAGGACAGGCCCCGGGCACTG
1510 1530 1550
CCTCACAGCCAAGGCTGGACTGGGTGGCTGCAGTGTGGTGTGTTAGTGGATAACCACATCG
1570 1590 1610
GAAGTGATTTTCTAAATTGGATTTGAATTCGGCTCCTGTTTTCTATTTGTCATGAAACAG
1630 1650 1670
TGTATTTGGGGAGATGCTGTGGGAGGATGTAAATATCTGTTTCTCCTCAAAAAAAAAA
1690
AAAAAAAAAAAAAAAAAAAAA

Figure 1B

Percent Similarity: 46.591 Percent Identity: 28.788

00340690-062999

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1 MEPPGDWGPWPWRSTPKTDVLRRLVLYLTFLGAPCYAPALPSCKEDEYPVG 50
      ...: ||. ... | .... .. ..|...: |
1 .....MVSLPRLCALWGCLLTAVHLGQCVTCSDKQYLHD 34
51 SECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCD 100
      ::||. | || |... |... | |...|...: |...: | | . | :
35 GQCCDLCQPGSRLTSHCTALEKTQCHPCDSGEFSAQWNREIRCHQHRHCE 84
101 PAMGLRASRNC SR TENAVCGCSPGHFCIVQGDHCAACRAYATSSPGQRV 150
      |. |||...: . . . ||. |...: |. . | |...: || |
85 PNQGLRVKKEGTAESDTVCTCKEGQHCTSKD...CEACAQHTPCIPGFGV 131
151 QKGGTESQDTLCQNCPPGTFSPNGTL.EECQHQT KC.SWLVTKAGAGTSS 198
      .: ||. ||: ||: ||. || .: | |. | . |. | . . . |||
132 MEMATETTDTVCHPCPVGFFSNQSSLFEKCYPWTSCEDKNLEVLQKGTSQ 181
199 SH.....WVWWFLSGSLVIVIVCSTVGLIICVKR..RKPRGDVVKVIV 239
      .: .: .: | .: |...: |...: |...: |...: |...: |...:
182 TNVICGLKSRMRALLVIPVVMGILITIFGVFLYIKKVVKPKDNEMLPPA 231
240 SVQRKRQEAEG.....EATVIEALQAPPDVTTVAVEETIPSFTGRSPNH 283
      . . . . || | : . |. | |...: || . . . |. | . | . . .
232 ARRQDPQEMEDYPGHNTAAPVQETLHGCQPVTQEDGKESRISVQERQVTD 281
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Figure 2

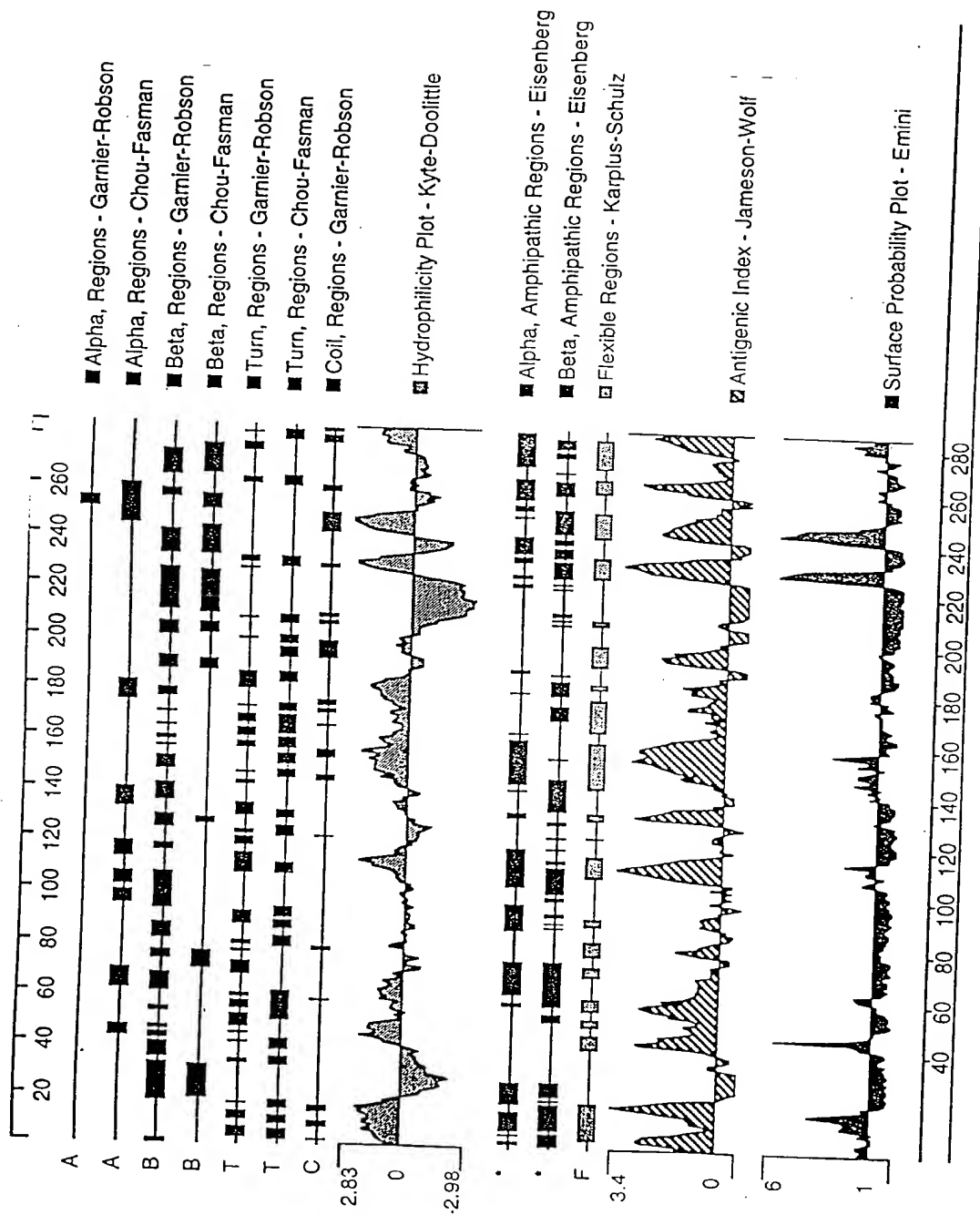


Figure 3

10 30 50
 CCCCCTTCTACAGGAAACCCGGAGTGGAGTGGAAACGGTGCAGGGGAGAACTCGCCCCCTC
 70 90 110
 CCATCGGGCGCCTCCTTCATACCGGCCCTTCCCCTCGGCTTTGCCTGGACAGCTCCTGCC
 130 150 170
 TCAGGCAGCGCCACCTGTGTGCGCCAGCGCCGCTCCACCCAGCAGGCCTGAGCCCCCTCTC
 190 210 230
 TGCTGCCAGACACCCCTGCTGCCCACTACTCCTGCTGCTCGGGTTCTGAGGCACAGCTT
 250 270 290
 GTCACACCGAGGCGGATTCTCTTTCTCTTTCTCTTTCTCTTCTGGCCCCACAGCCGAGCA
 310 330 350
 ATGGCGCTGAGTTCTCTGCTGGAGTTCATCCTGCTAGCTGGGTTCCCGAGCTGCCGGTC
 370 390 410
 TGAGCCTGAGTCATGGAGCCTCCTGGAGACTGGGGGCCTCCTCCCTGGAGATCCACCCCC
 430 450 470
 AGAACCGACGTCTTGAGGCTGGTGCTGTATCTCACCTTCCTGGGAGCCCCCTGCTACGCC
 490 510 530
 CCAGCTCTGCCGTCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGCTGCCCCAAG
 550 570 590
 TGCAGTCCAGGTTATCGTGTGAAGGAGGCGCTGCGGGGAGCTGACGGGCACAGTGTGTGAA
 610 630 650
 CCCTGCCCTCCAGGCACCTACATTGCCACCTCAATGGCCTAAGCAAGTGTCTGCAGTGC
 670 690 710
 CAAATGTGTGACCCAGATATTGGTTCCCCCTGTGACCTCAGGGGAAGAGGTCACCTGGAG
 730 750 770
 GCTGGTGCCACCTGAGTCCAGGCAGACAGAAAGGGGAACCAGACCCAGAGGTGGCCTTT
 790 810 830
 GAGTCACTGAGCGCAGAGCCTGTCCATGCGGCCAACGGCTCTGTCCCCTTGGAGCCTCAT
 850 870 890
 GCCAGGCTCAGCATGGCCAGTGCTCCCTGCGGCCAGGCAGGACTGCACCTGCGGGACAGG
 910 930 950
 GCTGACGGCACACCTGGGGGCAGGGCCTGAGCCTACAGGGAGGCACAGGGCAGGTGGGCT
 970 990 1010
 AGCCATGAACAGAAGAGGAAGCTGGAGTGCTTTGGGGGTTTCATGCATGTAGGCTGGGATT

Figure 4A

00340690 06904E60

1030	1050	1070
TGGGGCTCACACCTCAACCTGCATGCCCCAGTTCCATGCCCCCTCCCCTCTTGTGAAAGCAC		
1090	1110	1130
CTGTCTACTTGGGCTGAGGATGTGGGGGCACAGGTGGCAGGTGAGGCTGCCCTCAGGAGG		
1150	1170	1190
GGCCCAGGCCCCAGCTTGTACCCACCTCCACCAGTACCTGAAGAAGTGGGGCTCTCACCC		
1210	1230	1250
TACCTGCCTCTGCCATTGGAATGGCCTGGTTTGCACAGATGGGAAACCCGTTTGAGGGGT		
1270	1290	1310
GGGTGTCTGGGTGGGCACGTGGGGCGAGGACCTGCCTGAGGGACCCCTGCCCTGGAAGTGA		
1330	1350	1370
CAGTGCAAGCTCGGCGTCCCTGCCCATCTGGGCAGAAGGCTGGTTTCTCCCATCAACGAAG		
1390	1410	1430
CCCTCCCAGGACCTTCCTGCAAGCCCTCGTCCCACACGCAGCTCTGCCGTCCCTTGGTGT		
1450	1470	1490
CCCTCCCGGCTCAGGTCCCTCCATGCTGGGTACCTCTGGGCACCTCGTTTGGCTGAGCCA		
1510	1530	1550
GGGGTTCAGCCTGGCAGGGCGCCCTGGCAGCAGTCCCTTGGCCTGTGGATGCTGTCTGGC		
1570	1590	1610
CTGTGGATGGTGTCCCGCCCTCCACGTACCCCTCTCACCCCTCCTCTTGGAATCCAGCC		
1630	1650	1670
ATGGGCCTGCGCGGAGCCGGAAGTGTCCAGGACAGAGAACGCCGTGTGTGGCTGCAGC		
1690	1710	1730
CCAGGCCACTTCTGCATCGTCCAGGACGGGACCCTGCGCCGCGTGCCGCGCTTACGCC		
1750	1770	1790
ACCTCCAGCCCCGGCCAGAGGGTGCAGAAGGGAGGCACCGAGAGTCAGGACACCCTGTGT		
1810	1830	1850
CAGAACTGCCCCCGGGGACCTTCTCTCCCAATGGGACCCTGGAGGAATGTCAGCACCAG		
1870	1890	1910
ACCAATTGGCCTAATCATATGTGTGAAAAGAAAGCCAAGGGGTGAGCACACGGTGGC		
1930	1950	1970
CCCATCAGGGTTCATGTCCCCAGCCGTACCTCTTGAGCTCTGTACCCCCAAGCCTGGG		
1990	2010	2030
AGGTGGCCCCAGAGCTTTTCCAGGATCCGCGGCTCCTCCCAGGGCAGCCACTGCAGGCTG		
2050	2070	2090
GGGCAGGTGTATGTAGTCAAGGTGATCGTCTCCGTCCAGCGGTAAGACAGGAGGCAGA		
2110	2130	2150
AGGTGAGGCCACAGTCATTGAGCCCTGCAGGCCCTCCGGACGTACCCACGGTGGCCGTG		
2170	2190	2210
GAGGAGACAATACCCTCATTCACGGGGAGGAGCCCAAACCACTGACCCACAGACTCTGCA		
2230	2250	2270
CCCCGACGCCAGAGATACCTGGAGAGACGGCTGCTGATAGAGGCTGTCCACCTGGCGAAA		
2290	2310	2330
CCACCGGAGCCCGGAGGCTTGGGGGCTCCGCCCTGGGCTGGTTTCCGTCTCCTCCAGTGG		
2350	2370	2390
AGGGAGAGGTGGTGGCCCTGCTGGTGGTAGAGCTGGGGACGCCACGTGCCATTCCCATGG		
2410	2430	2450
TTCAGTGAGGGGCTGGTGGCCTCTGTTCTGCTGTGGCCTGAGCTCCCCAGAGTCTGAGG		
2470	2490	2510
AGGAGCCCCAGTTGCCCCCTCGCTCACAGACCACACACCCAGCCCTCCTGGGCCAACCCAG		
2530	2550	2570
AGGCCCCCTTCAGACCCCAGCTGTCTGCGCGTCTGACTCTTGTGGCCTCAGCAGGACAGGC		
2590	2610	2630
CCCGGGCACTGCCTCACAGCCAAGGCTGGAATGGGTGGCTGCAGTGTGGTGTAGTGG		
2650	2670	2690
ATACCACATCGGAAGTGATTTTCTAAAAATTGGATTTGAATTCGGAAAAAAA		

Figure 4B

Percent Similarity: 47.541 Percent Identity: 24.590

```

1 MEPPGDWGPPPWSTPRTDVLRLVLYLTFLGAPCYAPALPSCKEDEY...P 48
  |.|.:|.: : .:.. |. :.| .|: :.: .|: || .
1 MAPVAVWAALAVGLELWAAHALPAQVAF...TPYAPEPGSTCRLREYYDQ 48
49 VGSECCPKCSPGYRVKEACGELTGTVCPCPPGTYYIAHLNGLSKCLQCQM 98
  .: ||.|.|||| :.| |.. :|||:|..:|..:| :..|| |.
49 TAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGS 98
99 ...CDPDIGSPCDLRGRGHL.....EAGAHLSQGRQKGEPDPE 133
  :.:..: |.:..: :.|.:|.: .|. |.:
99 RCSSDQVETQACTREQNRICRTPGWYCALSKQEGCRLCAPLRKCRPGFG 148
134 VA.....FESLSAEPVHAANGS 150
  || :.: | |.:|.: :.
149 VARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDA 198
151 VPLEPHARLSMASAPC..GQAGLHLRDRADGTPGGRA..... 185
  |. .: : |||.:.. :|.: :.:..:|.:..:
199 VCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLPMGPS 248

```

Figure 5

09240690 062990

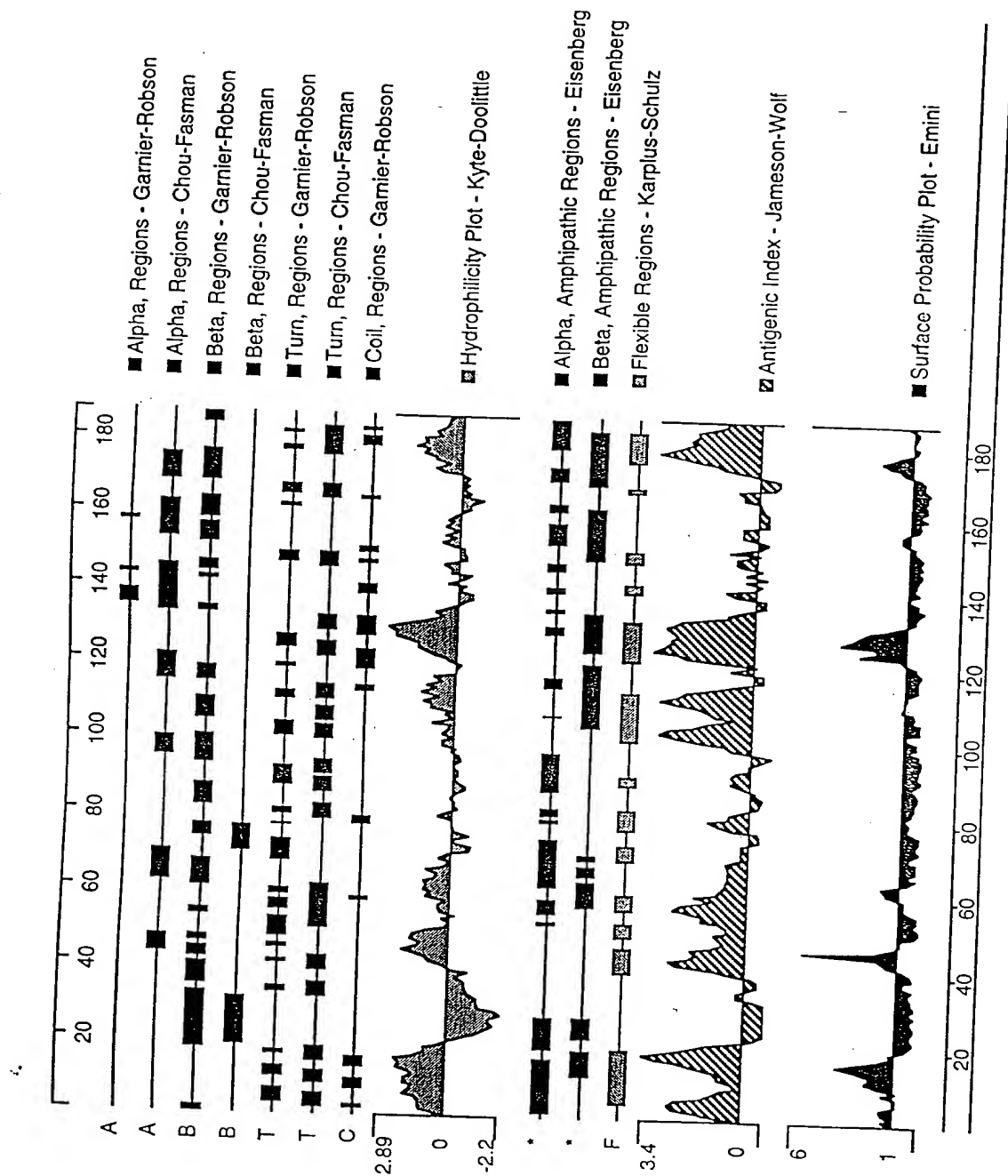


Figure 6

06290-0690+60

10 30 50
AAAGCTCGGGCTCCACCGGGGACGACCGCTCCTAGAACTGAGTGGTATCCCCGGGCGCT
70 90 110
GCAGGAATTCCAACCTGCCTGAAGGGACCCTGCCCTGGAAGTACAGTGCAAGCTCGGCG
130 150 170
TCCTGCCCATCTGGGAAGAAGGCTGGTTTCTCCCATCAACGAAGCCCTCCCAGGACCTTC
190 210 230
CTGCAAGCCCTCGTCCCACACGCAGCTCTGCCGTCCCTTGGTGTCCCTCCCGGCTCAGG
250 270 290
TCCTCCATGCTGGGTACCTCTGGGCACCTCGTTTGGCTGAGCCAGGGGTTTACGCTGGCA
310 330 350
M L G T S G H L V W L S Q G F S L A
GGGCGCCCTGGCAGCAGTCCTTGGCCTGTGGATGCTGTCTTGGCCTGTGGATGGTGTCCC
370 390 410
G R P G S S P W P V D A V L A C G W C P
GGCCTCCACGTACCCCTCTCAGCCCTCCTCTTGGACTCCAGCCATGGGCTGCGCGCG
430 450 470
G L H V P P L S P S S W T P A M G L R A
AGCCGGAAGTGTCCAGGACAGAGAACCGGTGTGTGGCTGCAGCCCAGGCCACTTCTGC
490 510 530
S R N C S R T E N A V C G C S P G H F C
ATCGTCCAGGACGGGGACCACTGCGCCGCGTGCCGCGCTTACGCCACCTCCAGCCCGGGC
550 570 590
I V Q D G D H C A A C R A Y A T S S P G
CAGAGGGTGCAGAAGGGAGGCACCGAGAGTCAGGACACCCTGTGTGCAAGTGCACCTG
610 630 650
Q R V Q K G G T E S Q D T L C Q N C P R
GGACCTTCTCTCCCAATGGGACCCTGGAGGAATGTCAGCACCAGACCAAGTAAGTGAACC
670 690 710
G P S L P M G P W R N V S T R P S K *
CGGGGGAGGCCAGCTCTGTGCCCTGGGGAGGGGGCTCCACGTTGCTTCCCTGGGAGATGA
730 750 770
CCGTCTTCTCCAGCAGAAAGGTTGAAGGTCCCACCCTGAGCGGCACCCTGGTCCATGCC
790 810 830
TGCGTCCAGGAGAGCTGCAGGTTGAAGCCTGTGTGCCCCAGATAACCCCTTCCATGGGCC
850 870 890
CAGACAAAGCCTCATCAGATCTGAGCTTCCCTGGAGGCTCAGGATGGGCCTTCCAGAAGC
910 930 950
AGGCCCAGAGGGAGGCTGCCTCCAGATCCCCTGTCCCCTGGGGCTGTGGGTGTCCCTGAA
970 990 1010
TGTCAGGGCCATGGGAGGGCCCCCTGGGCTTACAGGGGTGGGGAAAGTGAACACTCTGCTC
1030 1050 1070
TTTGTCCACCTTCCGGGAGGACAACCTTCAAATGCTGACCCTGGGCCCCCTAACTGACCTGA
1090 1110 1130
GACTTCAGAGCTTCTTGGGAGGAGCTGGGGTCCCCCAGCGGAGCCTGGGATGGAGCAGGG
1150 1170 1190
ATGGCTGCCCCAGGGAGGGGGCGGTGGGGCCTTCCATCCTGCTCTGCCCTCCTCGTCCTC
1210 1230 1250
TGGCCCCAGCTCAGTCCTGTCCATCTCCAGCTCTAACCATTGTGGCCCGACACTGGCTC
1270 1290 1310
TCCCTCTACCTTCTGTCTTGTCTGACACTGGTCTCCCGTGCTCTGGGGTCTCTGCACTG
1330 1350 1370
ATGGCTGCCTCCCGCTTCTCTCCCTCTCCCTCTGCCGTCTGTCTCCTGTGGCCAGTCT

Figure 7A

09340690-06904E60

1390	1410	1430
CTCCTTGTCTTCTCTCTCCTCCTTCTCTCTCCACCTCCCCATAGCCGAGCTTGGA		
1450	1470	1490
GTCAGACAGACCTCTGAGGTCTCATCCTGGAGCTGCCACCAGCCCAGCCTCCCTGGGACC		
1510	1530	1550
TGTCTTCACTGCCTGGGGCCCTGGGAGCCAGGGAGGCTCCCTGAGGCTGAGTGAACACTG		
1570	1590	1610
GGCGCTGCACCTGCCTCTCCACGTCCTCGGCCCCACTCCCGCAGGTGCAGCTGGCTGGT		
1630	1650	1670
GACGAAGCCCGGAGCTGGGACCAGCAGCTCCCACTGGGTATGGTGGTTTCTCTCAGGGAG		
1690	1710	1730
CCTCGTCATCGTCATTGTTTGCTCCACAGTTGGCCTAATCATATGTGTGAAAAGAAGAAA		
1750	1770	1790
GCCAAGGGGTGATGTAGTCAAGGTGATCGTCTCCGTCCAGGTATTGATCCTCCTCCCCCT		
1810	1830	1850
CTCCCTCCCCCTCCACCTTCCACCTCCCCTCTCCCCGCTGGGGCTGGTGTCTTCTGGTG		
1870	1890	1910
TACATGGTGGGGGCTCCCAGTTCTCTGAGGGTCTGAGTCTTTCAAGTACGCCACGGTA		
1930	1950	1970
GCTCAGGAAAGAACCCACCCCTCAAAGTGAAGCAGTAAATGAACCCGAGAACCTGGA		
1990	2010	2030
GTCCCAGGGGGGCTGAGCAGGCAGGGTCTCCACGATTCTGTGCTCACAGCGGGAAAAG		
2050	2070	2090
ACAGGAGGCAGAAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCTCCGGACGTCAC		
2110	2130	2150
CACGGTGGCCGTGGAGGAGACAATACCCTCATTCACGGGGGAGGAGCCCAAACCACTGAC		
2170	2190	2210
CCACAGACTCTGCACCCCGACGCCAGAGATACCTGGAGCGACGGCTGCTGAAAGAGGCTG		
2230	2250	2270
TCCACCTGGCGAAACCACCGGAGCCCGGAGGTTTGGGGGCTCCGCCCTGGGCTGGTTTCC		
2290	2310	2330
GTCTCCTCCAGTGGAGGGAGAGGTGGGGCCCCCTGCTGGGGTAGAGCTGGGGACGCCACGT		
2350	2370	2390
GCCATTCCCATGGGCCAGTGAGGGCCTGGGGCCTCTGTTCTGCTGTGGCCTGAGCTCCCC		
2410	2430	2450
AGAGTCCTGAGGAGGAGCGCCAGTTGCCCTCGCTCACAGACCACACACCCAGCCCTCCT		
2470	2490	2510
GGGTCCAGCCCAGAGGGCCCTTCAGACCCAGCTGTCTGCGCGTCTGACTCTTGTGGCCT		
2530	2550	2570
CAGCAGGACAGGCCCCGGGCACTGCCTTCAAGCCAAGGCTGGACTGGGTTGGCTGCAGTG		
2590	2610	2630
TGGTGTCTTAGTGGATACCACATCGGAAGTGATTTTCTAAATTGGATTGAAAAAAA		

Figure 7B

Percent Similarity: 45.522 Percent Identity: 26.866

```

1  MLGTSGHLVWLSQGFSL.....AGRPGSSPWPVD..... 29
   : : : : | : | : | : | : | : | : | : | : | :
1  .MAPVAVWAALAVGLELEWAAHALPAQVAFTPYAPEPGSTCRLREYYDQT 49
30 AVLACGWC .PGLHV.....PPLSPSSW 50
   | : | : | : | : | : | : | : | : | :
50 AQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSR 99
51 TPAMGLRASRNC SRTE NAVCGCSPGHFCIVQGDHCAACRAYATSSPGQR 100
   . . . . | : | : | : | : | : | : | : | : | :
100 CSSDQV .ETQACTREQNRIC TCRPGWYCALS KQEGCRLCAPLRKCRPGFG 148
101 VQKGGTESQDTLCQNCPRGSLPMGPWRNVSTRPSK..... 136
   | : | : | : | : | : | : | : | : | :
149 VARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDA 198

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Figure 8

00340690-062990

06904E60

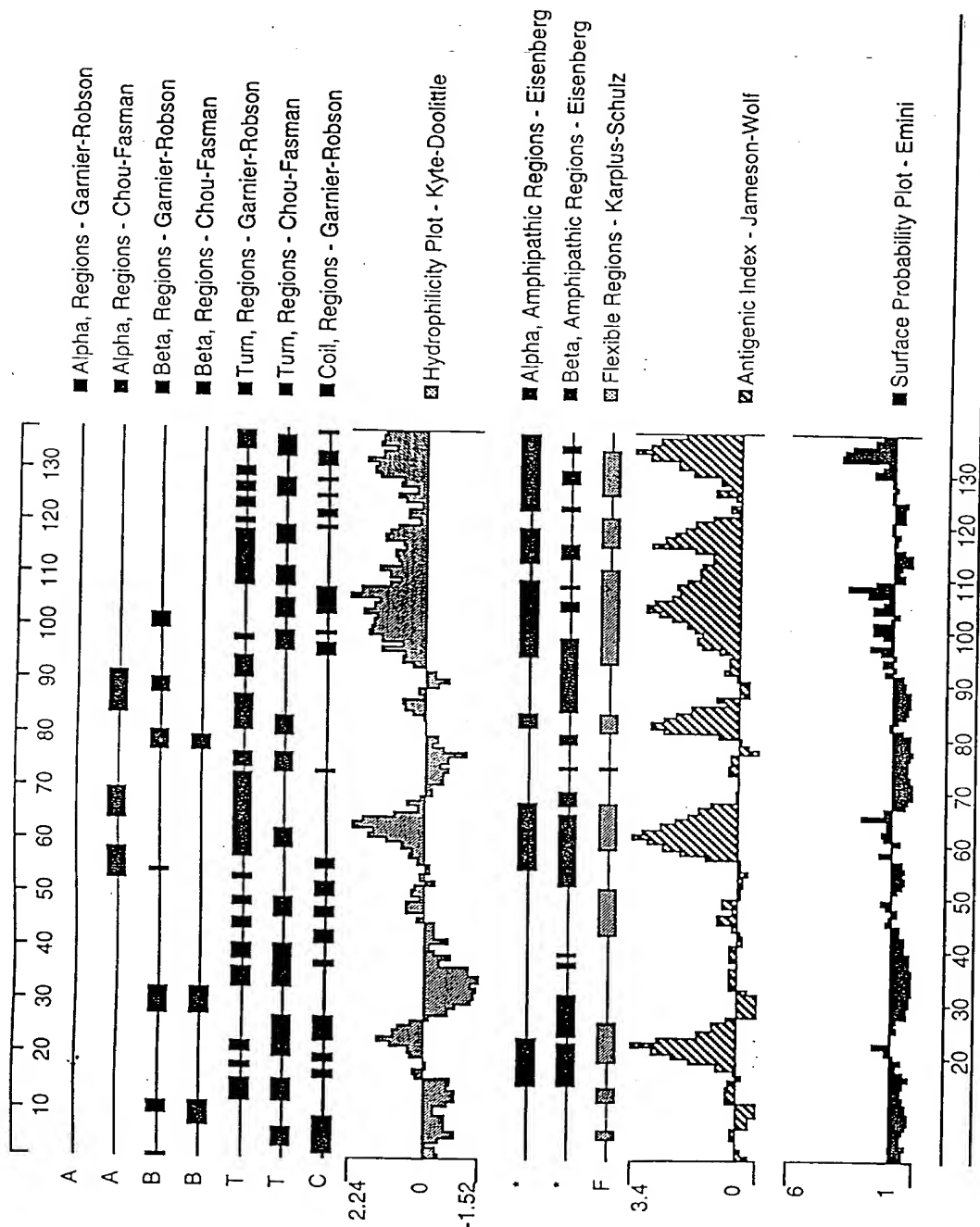


Figure 9

09340690-062999

Percent Similarity: 73.370 Percent Identity: 59.783

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1 MEPPGDWGPPPWSTPKTDVLRVLVLYLTFLGAPCYAPALPSCKEDEYPVG 50
|||||
1 MEPPGDWGPPPWSTPRTDVLRVLVLYLTFLGAPCYAPALPSCKEDEYPVG 50
51 SECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCD 100
101 PAMGLRAS.RNCSRTENAVCGCSPGHFCIVQGDGDHCAACRAYATSSPGQR 149
|.:.| . . . |. :. |. :. :|:. :. :. :. :. |.:. |:.
101 PDIGSPCDLRGRGHLEAG.....AHLSPGRQKGEPDPEVAFESLSAEPV 144
150 VQKGGTESQDTLCQNCPPGTFSPNGTLEECQHQTKCSWLVTKAGAGTSSS 199
. . |. . . . :. :. :. :. |. |. :|:. :. :.
145 HAANGSVPLEPHARLSMASAPCGQAGLH.....LRDRADGTPGGR 184
200 HWVWWFSLGSLVIVIVCSTVGLIICVKKRKPRGDVVKVIVSVQRKRQEAE 249
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Figure 10

Percent Similarity: 70.588 Percent Identity: 60.294

```

1 MEPPGDWGPWPWRSTPKTDVLRRLVLYLTFLGAPCYAPALPSCKEDEYPVG 50
1 .....MLGTSGLVWLSQGFSLAGRPGSSP.....WPVD 29
51 SECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCMCD 100
30 AVLACGWCPGLHV.....PPLSPSSW.....T 51
101 PAMGLRASRNC SRTE NAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRV 150
52 PAMGLRASRNC SRTE NAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRV 101
151 QKGGTESQDTLCQNCPPGTFSPNGTLEECQHQTCSWLVTKAGAGTSSSH 200
102 QKGGTESQDTLCQNCPRGPSLPMGPWRNV..STRPSK..... 136

```

Figure 11

00340690-062999

09340690-062999

Percent Similarity: 37.984 Percent Identity: 20.155

```
1 MEPPGDWGPWPWRSTPRTDVLRVLVLYLTFLGAPCYAP.....ALPSCK 43
      .....|   ::| |. .|   |..|.
1 .....MLGTSGHLVWLSQGFSLAGRPGSSPWPVDAVLACGWCP 38
44 EDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKC 93
      . . |. |:: . . |. |. .|: . .|:::|. :| ::. .|
39 GLHVPPLSPSSWTPAMGLRASRNC SR TENAVCGCSPGHFCI..VQGDHC 86
94 LQCMCDPDIGSPCDLRGRGHLEAGAHLS PGRQKGEPDPEVAFESLSAEP 143
      .|. . . :||. :. | |... |:.. :. :. :|. |
87 AACRAYAT..SSPGQRVQKGGTESQDTLCQNCPRGPSLPMGPWRNVSTRP 134
144 VHAANGSVPLEPHARLSMASAPCGQAGLHLRDRADGTPGGRA. 185
135 SK.....|
      ..... 136
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Figure 12

[illegible]

Figure 13A

1650 CAGGACAGAGAACGCCGTGTGTGGCTGCAGCCCAGGCCACTTCTGCATCG 1699
 650 TCCAGGACGGGGACCACTGCGCCGCGTGCCGCGCTTACGCCACCTCCAGC 699
 1700 TCCAGGACGGGGACCACTGCGCCGCGTGCCGCGCTTACGCCACCTCCAGC 1749
 700 CCGGGCCAGAGGGTGCAGAAGGGAGGCACCGAGAGTCAGGACACCCCTGTG 749
 1750 CCGGGCCAGAGGGTGCAGAAGGGAGGCACCGAGAGTCAGGACACCCCTGTG 1799
 750 TCAGAACTGCCCCCGGGGACCTTCTCTCCCAATGGGACCCTGGAGGAAT 799
 1800 TCAGAACTGCCCCCGGGGACCTTCTCTCCCAATGGGACCCTGGAGGAAT 1849
 800 GTCAGCACCAGACCAAGTG..... 818
 1850 GTCAGCACCAGACCAATTGGCCTAATCATATGTGTGAAAAGAAGAAAGCC 1899
 819 CAGCTGGCTGGTGACGAAGGCCGAGCTGGG.....ACCAGCAGCTC 860
 1900 AAGGGGTGAGCACACGGTGGCCCCATCAGGGTTCATGTCCCCAGCCGTCA 1949
 861 CCACTGGGTATGGTGGTTTCTCTCAGGGAGCCTCGTCATCGTCATTGTTT 910
 1950 CCTCTTGGAGCTCTGTACCCCAAGCCTGGGAGGTGGCCCCAGAGCTTTT 1999
 911 GCTCCACAGTTGGCCTAATCATATGTGTGAAAAGAAGAAAGCCAAGGGGT 960
 2000 CCAGGATCCGCGGCTCCTCCCAGGGCAGCCACTGCAGGCTGGGGCAGGTG 2049
 961 GATGTAGTCAAGGTGATCGTCTCCGTCCAGCGG.AAAAGACAGGAGGCAG 1009
 2050 TATGTAGTCAAGGTGATCGTCTCCGTCCAGCGGTAAAAGACAGGAGGCAG 2099
 1010 AAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCTCCGGACGTCACC 1059
 2100 AAGGTGAGGCCACAGTCATTGA.GCCCTGCAGGCCCTCCGGACGTCACC 2148
 1060 ACGGTGGCCGTGGAGGAGACAATACCCTCATTACGGGGAGGAGCCCCAAA 1109
 2149 ACGGTGGCCGTGGAGGAGACAATACCCTCATTACGGGGAGGAGCCCCAAA 2198
 1110 CCACTGACCCACAGACTCTGCACCCCGACGCCAGAGATACCTGGAGCGAC 1159
 2199 CCACTGACCCACAGACTCTGCACCCCGACGCCAGAGATACCTGGAGAGAC 2248
 1160 GGCTGAATGAAAGAGGCTGTCCACCTGGCGGAACCACCGAGCCCGGAGG 1209
 2249 GGCTG.CTGATAGAGGCTGTCCACCTGGCGAAACCACCGAGCCCGGAGG 2297
 1210 CTTGGGGGCTCCACCCTGGACTGGCTTCCGTCTCCTCCAGTGGAGGGAGA 1259
 2298 CTTGGGGGCTCCGCCCTGGGCTGGTTTCCGTCTCCTCCAGTGGAGGGAGA 2347
 1260 GGTGGCGCCCTTGCTGG.GGTAGAGCTGGGGACGCCACGTGCCATTCCCA 1308
 2348 GGTGGTGCCCTTGCTGGTGGTAGAGCTGGGGACGCCACGTGCCATTCCCA 2397

Figure 13B

[illegible]

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1 .....GCACGAGCTGCCTCCCGCAGGCGC 24
    | | | | |
701 GTTGCTTCCCTGGGAGATGACCGTCTTCTCCAGCAGAAAGGTTGAAGGTC 750
    | | | | |
25  CACCTGTGTCCCCCAGCGCCGCTCCACCCAGCAGGCCTGAGCCCCCTCTCT 74
    | | | | |
751 CCACCCTGAGCGGCACCCTGGTCACATGCCTGCGTCCAGGAGAGCTGCAG 800
    | | | | |
75  GCTGCCAGACACCCCTGCTGCCCCACTCTCCTGCTGCTCGGGTTCTGAGG 124
    | | | | |
801 GGTGAAGCCTGTGTGCCCCAGATAACCCCTTCCATGGGCCCAGACAAAGC 850
    | | | | |
125 CACAGCTTGTACACCGAGGCGGATTCTCTTTCTCTTTCTTTCTCTTCT 174
    | | | | |
851 CTCATCAGATCTGAGCTTCTGAGGCTCAGGATGGGCCTTCCCAGAAGC 900
    | | | | |
175 TGGCCCACA.....GCCGCAGCAATGGCGCTGAGTTCCTCTGCTGGAGTT 219
    | | | | |
901 AGGCCCAGAGGGAGGCTGCCTCCAGATCCCCTGTCCCCTGGGGCTGTGGG 950
    | | | | |
220 CATCCTGCTAGCTGGGTTCCTGAGCTGCCGGTCTGAGCCTGAGGCATGGA 269
    | | | | |
951 TGTCCCTGAATGTCAGGGCCATGGGAGGGCCCCCTGGGCTTCAGGGGTTGG 1000
    | | | | |
270 GCCTCCTGGAGACTGGGGGCTCCTCC.....CTGGAGATCCACCCCCAA 314
    | | | | |
1001 GGAAAGTGAACACTCTGCTCTTTGTCCACCTTCGGGAGGACAACCTTCAA 1050
    | | | | |
315 A.....ACCGACGTCTTGAGGCTGGTGTGTATCTCACCTTCCTGGGA 357
    | | | | |
1051 ATGCTGACCCTGGGCCCCCTAACTGACCTGAGACTTCAGAGCTTCTTGGGA 1100

```

Figure 14A


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2001 GGCAGGGTCTCCACGATTCGTGTGCTCACAGCGGGAAAAGACAGGAGGCA 2050
1009 GAAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCCCTCCGGACGTCAC 1058
2051 GAAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCCCTCCGGACGTCAC 2100
1059 CACGGTGGCCGTGGAGGAGACAATACCCTCATTAC .GGGGAGGAGCCCA 1107
2101 CACGGTGGCCGTGGAGGAGACAATACCCTCATTACGGGGGAGGAGCCCA 2150
1108 AACCCTGACCCACAGACTCTGCACCCCGACGCCAGAGATACCTGGAGCG 1157
2151 AACCCTGACCCACAGACTCTGCACCCCGACGCCAGAGATACCTGGAGCG 2200
1158 ACGGCTGAATGAAAGAGGCTGTCCACCTGGCGGAACCACCGGAGCCCCGA 1207
2201 ACGGCTG .CTGAAAGAGGCTGTCCACCTGGCGAAACCACCGGAGCCCCGA 2249
1208 GGCTTGGGGGCTCCACCCTGGACTGGCTTCCGTCTCCTCCAGTGGAGGGA 1257
2250 GGTTTGGGGGCTCCGCCCTGGGCTGGTTTCCGTCTCCTCCAGTGGAGGGA 2299
1258 GAGGTGGCGCCCCCTGCTGGGGTAGAGCTGGGGACGCCACGTGCCATTCCC 1307
2300 GAGGTGGGGCCCCCTGCTGGGGTAGAGCTGGGGACGCCACGTGCCATTCCC 2349
1308 ATGGGCCAGTGAGGGCCTGGGGCCTCTGTTCTGCTGTGGCCTGAGCTCCC 1357
2350 ATGGGCCAGTGAGGGCCTGGGGCCTCTGTTCTGCTGTGGCCTGAGCTCCC 2399
1358 CAGAGTCCTGAGGAGGAGCGCCAGTTGCCCCCTCGCTCACAGACCACACAC 1407
2400 CAGAGTCCTGAGGAGGAGCGCCAGTTGCCCCCTCGCTCACAGACCACACAC 2449
1408 CCAGCCCTCCTGGG .CCAACCCAGAGGG .CCTTCAGACCCAGCTGTGTG 1455
2450 CCAGCCCTCCTGGGTCCAGCCCAGAGGGCCCTTCAGACCCAGCTGTCTG 2499
1456 CGCGTCTGACTCTTGTGGCCTCAGCAGGACAGGCCCCGGGCACTGCCTCA 1505
2500 CGCGTCTGACTCTTGTGGCCTCAGCAGGACAGGCCCCGGGCACTGCCTTC 2549
1506 CAGCCAAGGCTGGACTGGGTGGCTGCAGTGTGGTGTGTTAGTGGATACCA 1555
2550 AAGCCAAGGCTGGACTGGGTGGCTGCAGTGTGGTGTGTTAGTGGATACCA 2599
1556 CATCGGAAGTGATTTTCTAAATTGGATTGGAATTCGGCTCCTGTTTTCTA 1605
2600 CATCGGAAGTGATTTTCTAAATTGGATTGAAAAAAAAA..... 2637

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Figure 14C

069290-06904660

Percent Similarity: 53.479 Percent Identity: 53.479

1 CCCCCTTCTACAGGAAACCCGGAGTGGACTGGAACGGTGCAGGGGGAGAA 50
|| | ||||| ||| | | | | | |

Figure 15A

[illegible]

Figure 15E

TNFR-I	V	C	PQGYIHPQNNSI	C	C	TK	C	HKGYLYND	C	PGPQDTD	C	R
TNFR-II	T	C	RLREYYDQTAQM	C	C	SK	C	SPGQHAQVF	C	TKTSDTV	C	D
CD40	A	C	REKQYLINSQ	C	C	SL	C	QPGQKLVSD	C	TEPTETE	C	L
4-1BB	-	-	-	-	-	SN	C	PAGTF	C	DNTRNQL	C	S
TR-2	S	C	KEDEYFVGSE	C	C	PK	C	SPGYRVKEA	C	GELTGTV	C	E

TNFR-I	E	C	ESGSFTASENHLRH	C	LS	C	SK	C	RKEMGOVEISS	C	TVDRDTV	C	G
TNFR-II	S	C	EDSTYTQLWNVPE	C	LS	C	GSR	C	SSDQVETQA	C	TREQNRI	C	T
CD40	P	C	GESEFLDTWNRETH	C	HQ	H	KY	C	DPNLGLRVQOK	G	TSETDTI	C	T
4-1BB	P	C	PENSESSAGGQRT	C	DI	C	RQ	C	KGVFTRKE	C	SSTSNAE	C	D
TR-2	P	C	PPGTYTAHLNGLSK	C	LQ	C	QM	C	DPAMGLRASRN	C	SRTENAV	C	G

TNFR-I	C	RIGQYRHYWSENLFQ	C	FN	C	SL	C	LNSTVHLS	C	QEKQNTV	C	T
TNFR-II	C	RPGWY	C	ALSKQEG	C	RL	C	APLRK	C	RPGFVAPP	G	TETSDV
CD40	C	EEGWH	C	TSEA	C	ES	C	VLHRS	C	SPGFGVKQIAT	G	VSDTI
4-1BB	C	TPGFH	C	LGAG	C	SM	C	EQD	C	KQGELTKKG	C	KD
TR-2	C	SPGHE	C	IVQGDH	C	AA	C	RAYAT	S	SPGQRVQXG	G	TESQDTL

TNFR-I	-	C	HAGFFFLRENE	C	VS	C	SN	C	KKSLE	C	TKL	C	L
TNFR-II	P	C	APGTFSTTSSTDI	C	RP	H	QI	C	NVVAIP	G	NASMDAV	C	T
CD40	P	C	FVGFFSNVSSAFEK	C	HP	N	TS	C	ETKDLVQQA	G	TNKTDV	C	G
4-1BB	-	C	F-GTFNKQKRG	C	RP	N	TN	C	SLDGKSVLVN	G	TKERDV	C	G
TR-2	N	C	PPGTFSPNGTLEE	C	QH	Q	TK	C	SWLYTKA	G	AGTSSSH	W	V

Figure 16